In the Specification:

Please amend the specification as follows.

On page 1 of the specification, please insert the following heading prior to the title of the invention at line 1:

-- TITLE OF THE INVENTION --

On page 1 of the specification, please insert the following paragraph immediately following the title of the invention:

-- CROSS-REFERENCE TO RELATED APPLICATIONS

The present application is a Continuation of International Patent Application No. PCT/EP00/03844, filed on April 27, 2000, which claims priority of German Patent Application No. 199 19 124.7, filed on April 21, 1999. --

On page 1 of the specification, please insert the following heading at line 14, immediately before the second full paragraph:

-- BACKGROUND OF THE INVENTION --

On page 3 of the specification, please insert the following heading at line 10, immediately before the second full paragraph:

-- BRIEF SUMMARY OF THE INVENTION --

On page 4 of the specification, please delete the paragraph extending from line 7 to line 17, and replace it with the following paragraph:

-- In microorganisms and plants, the biosynthesis of aromatic amino acids proceeds firstly through 7 enzyme-catalysed reactions of the shikimate pathway from erythrose-4-phosphate and phosphoenol pyruvate to chorismate (figure 1). Chorismate is the substrate of the first branching point. In the baker's yeast Saccharomyces cerevisiae, starting from this branching point, on the one hand anthranilate is formed via the enzyme anthranilate synthase (E.C. 4.1.3.27), and on the other prephenate via the enzyme chorismate mutase (E.C. 5.4.99.5). Finally, via further intermediate products, tyrosine and phenylalanine are formed from prephenate (Braus, 1991). In the baker's yeast Saccharomyces cerevisiae, the chorismate mutase is encoded by the ARO7 gene (Schmidheini et al., 1989), which is located on chromosome XVI. ARO7 encodes a 0.95 kb mRNA and contains a 771 bp open reading frame, which codes for a protein consisting of 256 amino acids. The present invention will be understood to include all chorismate mutases, including fragments, variants and homologs thereof, except for Saccharomyces cerevisiae ARO7 chorismate mutase. --

On page 4 of the specification, please insert the following heading at line 21, immediately before the third full paragraph:

-- DETAILED DESCRIPTION --

On page 14 of the specification, please delete the paragraph extending from line 6 to line 13, and replace it with the following paragraph:

-- A BglII digestion of genomic DNA from *Hansenula polymorpha* and subsequent Southern Blot analysis with a chorismate mutase-specific probe such as e.g. SEQ ID NO:3 gave two band of 3.2 kb and 3.0 kb respectively. Further investigation

showed that the 3.2 ~~kg~~ kb BglII/BglII fragment includes 690 bp of SEQ ID NO:3 and contains the flanking 5' region. The 3.0 ~~bp~~ kb BglII fragment includes 960 bp of SEQ ID NO:3 and contains the flanking 3' region. The isolation and directed fusion of the 3.2 kb fragment with the 3.0 kb fragment by means of standard procedures known to the skilled person leads to a 6.2 kb fragment, which includes the chorismate mutase gene and large 5' and 3' flanking regions. --

On page 17 of the specification, please insert the following heading at line 12, immediately before the line beginning with the words, "Figure 1 shows...":

-- BRIEF DESCRIPTION OF THE DRAWINGS --